

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 25, 2000, 03:51:15 ; Search time 853.82 Seconds
(without alignments)
3410.674 Million cell updates/sec

Title: US-09-373-230-1
Perfect score: 471
Sequence: 1 AACCTTGCCGCGACTTCACTG.....TCACTAAGTTACATCAAGT 471

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
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14: gb_est14:*
15: gb_est15:*
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18: gb_est18:*
19: gb_est19:*
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21: gb_est21:*
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42: em_estfun:*
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118: gb_gss19:*
119: em_gss13:*
120: gb_gss20:*
121: gb_gss21:*
122: gb_gss22:*
123: gb_gss23:*
124: gb_gss24:*
125: em_gss14:*
126: em_gss15:*
127: em_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465.8	98.9	603	AA930362	AA930362 VS59f07.r
2	400.6	85.1	646	AA892285	AA892285 EST196088
3	365.6	77.6	512	AA125102	AA125102 UI-M-BH2.
4	337.6	71.7	474	AA121020	AA121020 ud69c02.x
5	308.6	65.5	434	AA237736	AA237736 mx29g01.r
6	274	58.2	469	AA1463005	AA1463005 vb89g05.x
7	260.8	55.4	423	AA558748	AA558748 L0299E02-
8	239.8	50.9	443	AA597984	AA597984 AV597984
9	208	44.2	357	AA049334	AA049334 UI-M-BH1-
10	207.4	44.0	369	AA1176343	AA1176343 EST219926
11	197.4	41.9	342	AA1835755	AA1835755 UI-M-A10-
12	191.6	40.7	335	AA066410	AA066410 AV066410
13	173.4	36.8	289	AA245600	AA245600 mx30a01.r
14	166.8	35.4	505	AA1046315	AA1046315 ud69c02.y
15	155.6	33.0	574	AA597985	AA597985 AV597985
16	153.8	32.7	294	AA072353	AA072353 AV072353
17	153.8	32.6	354	AA1642457	AA1642457 vv80b10.x
18	153.4	32.6	292	AA063007	AA063007 AV063007
19	151.6	32.2	287	AA065008	AA065008 AV065008
20	148.4	31.5	276	AA078115	AA078115 AV078115
21	148	31.4	285	AA032583	AA032583 AV032583
22	144	30.6	306	AA069911	AA069911 AV069911
23	142.4	30.2	300	AA169683	AA169683 AV169683
24	139.4	29.6	300	AA239413	AA239413 AV239413
25	138.4	29.4	294	AA067717	AA067717 AV067717
26	138	29.3	299	AA067682	AA067682 AV067682
27	135.6	28.8	293	AA076434	AA076434 AV076434
28	130.4	27.7	279	AA087765	AA087765 AV087765
29	124.8	26.5	281	AA062592	AA062592 AV062592
30	124.8	26.5	567	AA062592	AA062592 AV062592
31	117.2	24.9	259	AA071444	AA071444 AV071444
32	114	24.2	549	AA151778	AA151778 xf69b11.x
33	92	19.5	515	AA1800476	AA1800476 tj14h05.x
34	78	16.6	655	AA0377384	AA0377384 RPC111-16
35	63.8	13.5	325	AA142292	AA142292 EST292531
36	57.2	12.1	188	AA077488	AA077488 AV077488
37	56.6	12.0	468	AA1129421	AA1129421 qc38g11.x
38	54.2	11.5	196	AA0328761	AA0328761 AV328761
39	49.6	10.5	309	AA83242	AA83242 K4692F Huma
40	47.6	10.1	438	AA1247015	AA1247015 qx52c10.x
41	42.8	9.1	188	AA069285	AA069285 AV069285
42	39.6	8.4	413	AA0592903	AA0592903 HS_5453_A
43	37.6	8.0	442	AA129391	AA129391 zn85b03.s
44	37.6	8.0	1101	AA063921	AA063921 Drosophila
45	37.4	7.9	751	AA0687654	AA0687654 NF011G05R

ALIGNMENTS

RESULT 1
AA930362

LOCUS AA930362 603 bp mRNA EST 23-APR-1998
DEFINITION VS59f07.r1 Strataene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:1150597 5' similar to gb:D49949 Mouse mRNA for IGF precursor
polypeptide (MOUSE);, mRNA sequence.
ACCESSION AA930362 GI:3079955
VERSION AA930362.1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 603)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
CONTACT: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:623805
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 445.
FEATURES
location/Qualifiers
1..603
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1150597"
/clone_lib="Strataene mouse skin (#937313)"
/sex="females"
/tissue="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dt. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3' t
BASE COUNT 197 a 111 c 132 g 163 t
ORIGIN
Query Match 98.9%; Score 465.8; DB 7; Length 603;
Best Local Similarity 99.2%; Pred. No. 1e-115;
Matches 467; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 AACCTTGCCGACTTCACGTACCAACCGCACTAATACGGAATATAATGACCAAGTCTC 60
Db 5 AACTTTGGCCGACTTCACGTACCAACCGCACTAATACGGAATATAATGACCAAGTCTC 64
QY 61 TTGCTTGACAAAGACAGCCTGTGTTCAGAGATATGACTGATATGATCAAAAGTGCAGT 120
Db 65 TTGCTTGACAAAGACAGCCTGTGTTCAGAGATATGACTGATATGATCAAAAGTGCAGT 124
QY 121 GAACCCGAGACGACTGATATATATATACATGATCAAAAGACAGTGAAGTAAGAGACTGGCT 180
Db 125 GAACCCGAGACGACTGAT 184
QY 181 GTGACCCCTCTGTGAAGGATAGTAATAAGTCTACCTCTCTGTGAAGCAAGATCATTT 240
Db 185 GTGACCCCTCTGTGAAGGATAGTAATAAGTCTACCTCTCTGTGAAGCAAGATCATTT 244
QY 241 TCCTTTGAGAAATGATCCACCTGAAAAATATGATGATATACAAAGTGTCTCATATTC 300

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Db 245 TCCTTGAGGAAATGGATCCACCTGAAATATATGATGATATACAAAGTGATCATATTC 304
QY 301 TTTCAGAAACGTTGCCAGACACACAAGATGAGTTGAATCTTCACGTATGAAGGA 360
Db 305 TTTCAGAAACGTTGCCAGACACACAAGATGAGTTGAATCTTCACGTATGAAGGA 364
QY 361 CACTTCTTGTGCTTGCCAAAAGGAGATGATGCTTTCAACCTCATCTTGAAAAAAGAGAT 420
Db 365 CACTTCTTGTGCTTGCCAAAAGGAGATGATGCTTTCAACCTCATCTTGAAAAAAGAGAT 424
QY 421 GAAAAATGGGATAAATCTGTAATGTTCACTCTCACTAATCATCAAGT 471
Db 425 GAAAAATGGGATAAATCTGTAATGTTCACTCTCACTAATCATCAAGT 475

RESULT 2
AA892285/c 646 bp mRNA EST 25-JAN-1999
LOCUS EST196088 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
DEFINITION RK1A060 3' end, mRNA sequence.
ACCESSION AA892285 GI:3019164
VERSION AA892285.1
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 646)
AUTHORS Lee,N.H., Glodok,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (RESE) Catalog & Rat
Gene Index
Unpublished (1998)
COMMENT Contact: Lee, NH
ATCC
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

FEATURES
Location/Qualifiers
source 1..646
/organism="Rattus sp."
/db_xref="ATCC (inhost):2017880"
/db_xref="taxon:10118"
/clone="RK1A060"
/clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT 177 a 126 c 123 g 220 t
ORIGIN
Query Match 85.1%; Score 400.6; DB 7; Length 646;
Best Local Similarity 91.8%; Pred. No. 4,4e-98;
Matches 434; Conservative 1; Mismatches 35; Indels 3; Gaps 1;

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Db 399 CTGTGACCCCTATCTGTGAAGGATGGAAGGATGTCTACCTCTCTGTAACCAAAATCA 340
QY 239 TTTCCTTGAGAAATGATCCACCTGAAATATATGATGATATACAAAGTGATCATAT 298
Db 339 TTTCCTTGAGAAATGATCCACCTGAAATATATGATGATATACAAAGTGATCATAT 280
QY 299 TCTTTGAGAAACCTGTGTCAGACACACAAGATGAGCTTGAATCTTCACTGTATGAAG 358
Db 279 TCTTTGAGAAACCTGTGTCAGACACACAAGATGAGCTTGAATCTTCACTGTATGAAG 220
QY 359 GACACTTCTGCTTGCCAAAAGGAGATGATGCTTTCAAACTCATCTTGAAAAAAGG 418
Db 219 GACACTTCTGCTTGCCAAAAGGAGATGATGCTTTCAAACTCATCTTGAAAAAAGG 160
QY 419 ATGAAATGGGATAAATCTGTAATGTTCACTCTCACTAATCATCAAGT 471
Db 159 ATGAAATGGGATAAATCTGTAATGTTCACTCTCACTAATCATCAAGT 107

RESULT 3
AM125102/c 512 bp mRNA EST 22-OCT-1999
LOCUS UI-M-BH2.1-1-apx-g-10-0-UI.s1 NIH_BMAP_M_S3.1 Mus musculus cDNA clone
DEFINITION UI-M-BH2.1-1-apx-g-10-0-UI 3', mRNA sequence.
ACCESSION AM125102
VERSION AM125102.1 GI:6100632
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 512)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized basal ganglia library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
The following repetitive elements were found in this cDNA sequence:
17-81, >MSTD#LTR/MaLR
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
Location/Qualifiers
source 1..512
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH2.1-1-apx-g-10-0-UI"
/clone_lib="NIH_BMAP_M_S3.1"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7P3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S3.1 library is a subtracted library of a
series, ultimately derived from a mixture of individually
tagged normalized libraries from ten regions of the mouse

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brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S3.1) was constructed as follows: PCR amplified cDNA inserts from NIH_BMAP_M_S2 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the NIH_BMAP_M_S2 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH_BMAP_M_S3.1 library. This procedure has been previously described (Bonaldi, Lennon and Soares, Genome Research 6:791-806, 1996)

TAG_LIB=NIH_BMAP_M_S3.1
TAG_TISSUE=basal-ganglia
TAG_SEQ=GTAC"

BASE COUNT 135 a 104 c 94 g 179 t
ORIGIN

Query Match 77.6%; Score 365.6; DB 20; Length 512;
Best Local Similarity 99.7%; Pred. No. 1.2e-88;
Matches 365; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 106 GATCAAGTGGCCAGTGAACCCAGACCACTGATATATACATGTACAAAGACAGTGAA 165
|||||
Db 512 GATCAAGTGGCCAGTGAACCCAGACCACTGATATATACATGTACAAAGACAGTGAA 453
|||||
QY 166 GTAAGAGAGCTGGCTGTGACCCCTCTGTGAAGATAGTAAAYGTCCTACCCCTCTCTGT 225
|||||
Db 452 GTAAGAGAGCTGGCTGTGACCCCTCTGTGAAGATAGTAAAYGTCCTACCCCTCTCTGT 393
|||||
QY 226 AAGAACAAGATCATTTCTTTGAGAAATGGATCCACCTGAAATATTTGATGATATACAA 285
|||||
Db 392 AAGAACAAGATCATTTCTTTGAGAAATGGATCCACCTGAAATATTTGATGATATACAA 333
|||||
QY 286 AGTATCTCATATTTCTTTGAGAAACGTTCCAGACACACACAAGATGGAGTTGATCT 345
|||||
Db 332 AGTATCTCATATTTCTTTGAGAAACGTTCCAGACACACACAAGATGGAGTTGATCT 273
|||||
QY 346 TCACTGTATGAAGACACTTTCTTGTGCTTCCCAAAAGAGATGATGCTTTCAAACTCAT 405
|||||
Db 272 TCACTGTATGAAGACACTTTCTTGTGCTTCCCAAAAGAGATGATGCTTTCAAACTCAT 213
|||||
QY 406 CTGAAAAAAGATGAATAATGGGATTAATCTGTATGTTCACTCTCACTAATTACAT 465
|||||
Db 212 CTGAAAAAAGATGAATAATGGGATTAATCTGTATGTTCACTCTCACTAATTACAT 153
|||||
QY 466 CAAAGT 471
|||||
Db 152 CAAAGT 147

RESULT 4
AI121020/c 474 bp mRNA EST 02-SEP-1998
LOCUS
DEFINITION ud69c02.x1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1451138 3' similar to gb:D49949 Mouse mRNA for IGF precursor polypeptide (MOUSE);, mRNA sequence.

ACCESSION AI121020 GI:3521344
VERSION AI121020.1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 474)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:924454

FEATURES
Seq primer: custom primer used
High quality sequence stop: 410.

Location/Qualifiers
1. 474

/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1451138"
/clone_lib="Sugano mouse liver mlia"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGGGCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCTTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTTAAAGCTGCG and 3' end primer CGACCTGCAGCTCGACACA."

BASE COUNT 132 a 97 c 83 g 162 t
ORIGIN

Query Match 71.7%; Score 337.6; DB 8; Length 474;
Best Local Similarity 99.7%; Pred. No. 4.4e-81;
Matches 337; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 134 GACTGATATATATACATGTACAAAGACAGTGAAGTGAAGAGACTGGCTGTGACCTCTCTG 193
|||||
Db 474 GACTGATATATATACATGTACAAAGACAGTGAAGTGAAGAGACTGGCTGTGACCTCTCTG 415
|||||
QY 194 TGAAGGATAGTAAAYGTCCTACCCCTCTCTGTAAAGACAAAGATCATTTCTTTGAGGAAA 253
|||||
Db 414 TGAAGGATAGTAAAYGTCCTACCCCTCTCTGTAAAGACAAAGATCATTTCTTTGAGGAAA 355
|||||
QY 254 TGGATCCACCTGAAAATATGTATATACAAAGTATCTCATATTTCTTTGAGGAAACGTG 313
|||||
Db 354 TGGATCCACCTGAAAATATGTATATACAAAGTATCTCATATTTCTTTGAGGAAACGTG 295
|||||
QY 314 TTCCAGGACACAAACAAGATGAGTTGATCTTCACTGTATGAAGACACTTCTTGTCTT 373
|||||
Db 294 TTCCAGGACACAAACAAGATGAGTTGATCTTCACTGTATGAAGACACTTCTTGTCTT 235
|||||
QY 374 GCCAAAAGAGATGATGCTTTCAAACTCATTTCTGAAAAAAGATGAATAATGGGATA 433
|||||
Db 234 GCCAAAAGAGATGATGCTTTCAAACTCATTTCTGAAAAAAGATGAATAATGGGATA 175
|||||
QY 434 AATCTGTAATGTTCACTCTCACTAATTACATCAAGT 471
|||||
Db 174 AATCTGTAATGTTCACTCTCACTAATTACATCAAGT 137

RESULT	5	AA237736	434 bp	mus musculus	EST	03-MAR-1997
LOCUS	AA237736					
DEFINITION	AA237736	434 bp	mus musculus	EST	03-MAR-1997	
ACCESSION	AA237736					
VERSION	AA237736.1	GI:1861775				
KEYWORDS	EST.					
SOURCE	house mouse.					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (mouse); mRNA sequence.					
AUTHORS	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisels, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.					
TITLE	The WashU-HMNI Mouse EST Project					
JOURNAL	Unpublished (1996)					
COMMENT	Contact: Marra M/Mouse EST Project WashU-HMNI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:421352 Putative full length read vector to vector length is 437 Seq primer: -28ml3 rev2 ET from Amersham.					
FEATURES	Location/Qualifiers					
SOURCE	1..434					
	/organism="Mus musculus"					
	/db_xref="taxon:10090"					
	/clone="IMAGE:681648"					
	/clone_lib="Soares mouse NML"					
	/tissue_type="liver"					
	/lab_host="DH10B"					
	/note="Vector: PT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGGAATCTTTTCTTTTCTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified PT7T3 vector. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."					
BASE COUNT	139 a 79 c 92 g 124 t					
ORIGIN						
Query Match	65.5%;	Score 308.6;	DB 2;	Length 434;		
Best Local Similarity	99.7%;	Pred. No. 3e-73;				
Matches 308;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;		
Db	163	GAAGTAAGAGGACTGGCTGTGACCCCTCTCTGTGAAGAGTAGTAAAYGTCTACCCCTCC	222			
Db	1	GAAAGTAAGAGGACTGGCTGTGACCCCTCTCTGTGAAGAGTAGTAAAYGTCTACCCCTCC	60			
Db	223	TGTAAGAACAAAGATCAATTCCTTTGAGGAATATGATCCACCTGAAATATATGATGATATA	282			
Db	61	TGTAAGAACAAAGATCAATTCCTTTGAGGAATATGATCCACCTGAAATATATGATGATATA	120			
Db	283	CAAGTGAATCTCATATCTTTTTCAGAAACGTGTTCCAGAGACACAAACAGATGAGATTGAA	342			
Db	121	CAAGTGAATCTCATATCTTTTTCAGAAACGTGTTCCAGAGACACAAACAGATGAGATTGAA	180			

QY	343	TCTTTCACGTGATGAAGGACACCTTTCTTGCTTGCCCAAAAGGAGATGATGCTTTCAAACTC	402
Db	181	TCTTCACGTATGAGGACACTTCTTGCTTGCCCAAAAGGAGATGATGCTTTCAAACTC	240
QY	403	ATTCTGAAAAGGATGAAAAATGGGGATAAATCTGTATGTTCACTCTCACTAACCTTA	462
Db	241	ATTCTGAAAAAAAAAGGATGAAAAATGGGGATAAATCTGTATGTTCACTCTCACTAACCTTA	300
QY	463	CATCAAACT 471	
Db	301	CATCAAACT 309	
RESULT	6		
A1463005/c			
LOCUS			
DEFINITION	A1463005	469 bp	mRNA EST 09-MAR-1999
	vb89g05.x1	Soares mouse 3nbms	Mus musculus cDNA clone IMAGE:764216
		3', similar to gb:D49949	Mouse mRNA for IGIF precursor polypeptide
	(MOUSE);	mRNA sequence.	
ACCESSION	A1463005		
VERSION	A1463005.1	GI:4317035	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 469)		
AUTHORS	Marta,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.		
TITLE	The WashU-NCI Mouse EST Project 1999		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Marta M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:465136 This clone was previously sequenced on the 5' end only, this new data is from the 3' end High quality sequence stop: 324.		
FEATURES			
source	Location/Qualifiers		
	1..469		
	/organism="Mus musculus"		
	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:764216"		
	/clone_lib="Soares mouse 3nbms"		
	/sex="male"		
	/tissue_type="Spleen"		
	/dev_stage="4 weeks"		
	/lab_host="DH10B"		
	/note="Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAGCTGGAGCGGCCGGCTGTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. RNA provided by Dr. Bertrand Jordan. library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."		
BASE COUNT	132 a	99 c	90 g 144 t 4 others
ORIGIN			
Query Match	58.2%;	Score 274;	DB 10; Length 469;
Best Local Similarity	90.7%;	Pred.No. 6.9e-64;	


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/clone="E1CA035C10"
/tissue_type="Bos taurus cartilage fetus"
/dev_stage="fetus"
/notes="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A
was deleted from a NotI site"
BASE COUNT      134 a      77 c      79 g      153 t
ORIGIN

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Query Match      50.9%; Score 239.8; DB 19; Length 443;
Best Local Similarity 75.5%; Pred. No. 1.2e-54;
Matches 324; Conservative 1; Mismatches 98; Indels 6; Gaps 2;

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QY 37 CGGAATATTAATGACCAAGTCTCTGTTGACAA--AAGACAGCCTGTGTTGAGGAT 93
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 443 CGAAATTTGAATGACCAAGTCTCTTCATTACCAAGGAAATCAACCTGTCTTTGAGGAT 384
QY 94 ATGACTGATATGATCAAGTGCAGTGAACCCAGACAGACAGATGATATATACATGTAC 153
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 383 ATGCTGATTTCTGACCTGTTACAGATTAATGACACCCAGACCAATTTATCATATATATGTAT 324
QY 154 AAAGACAGTGAAGTGAAGAGAGCTGGCTGTGACCTCTCTGTGAGAGATAGTAAAYGCT 213
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 323 AAGGACAGCCTCAGTGAAGAGTGGCCCTAACCATCTCTGTGAGAGTGAAGAAATGTCT 264
QY 214 ACCCTCTCTCTGTAAGACCAAGATCATTTCTTTGAGGAATGATCCACCTGAAATATTT 273
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 263 ACTCTCTCTCTGTAAGACCAAAATGTTCTTTAAGGAATGATTCCTCTGATTAACATTT 204
QY 274 GATGATATACAAAGTGAATCTCATATTTCTTCAAGAAAGTGTCCAGAGAC--ACAACAG 330
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 203 GATTAATGAAGAAAGTGAATCATATTTCTTCAAGAAAGTGTCCAGAGACATGATTAAG 144
QY 331 ATGAGTTTGAATCTTCACCTGTATGAGAGACACTTTCTTGTCCCAAAAGAGAGATGAT 390
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 ATACAATTTGAGTCTTCAATTTGTACAAAGGGTACTTTCTAGCTGTAAAGAAAGCAATGAC 84
QY 391 GCTTCAAACTCATTTCTGAAAAAAGGATGAAGATGGGATTAATCTGTAATGTTCACT 450
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 CTTTCAAACTCATTTCTGAAAAAAGGATGATTAAGATTAATCTGTAATGTTCACT 24
QY 451 CTCACCTAAC 459
   ||| |||
Db 23 GTTCAAAAC 15

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RESULT 9
AM049334/c 357 bp mRNA EST 18-SEP-1999
LOCUS
DEFINITION
UI-M-BH1-amr-f-09-0-UI_s1 NIH_BMAP_M_S2 Mus musculus cDNA clone
UI-M-BH1-amr-f-09-0-UI 3', mRNA sequence.
ACCESSION
AM049334
VERSION
AM049334.1 GI:5909863
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 357)
AUTHORS
Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
COMMENT
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
The sequence contained an oligo-dT track that was present in the

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oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized brain stems library cDNA library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: 18-84, >MSTP#LTR/MaLR
Seq primer: M13 Forward
POLYA=Yes.

FEATURES

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source
location/Qualifiers
1..357
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH1-amr-f-09-0-UI"
/clone_lib="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S2 library is a subtracted library derived from
NIH_BMAP_M_S1, which in turn is a subtracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
ganglia, pineal gland, striatum, hippocampus). The driver
used for subtraction consisted of a pool of 5,000 clones
from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
obtained from non-normalized and normalized mouse brain
spinal cord libraries.
TAG_LIB=NIH_BMAP_M_S2
TAG_TISSUE=brain-stems
TAG_SEQ=TCATG"
BASE COUNT      100 a      71 c      59 g      127 t
ORIGIN

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Query Match      44.2%; Score 208; DB 19; Length 357;
Best Local Similarity 100.0%; Pred. No. 4.5e-46;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 264 TGAATAATTTGATGATATACAAAGTGAATCTCATATTTCTTCAAGAAACGTGTTCCAGACA 323
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 357 TGAATAATTTGATGATATACAAAGTGAATCTCATATTTCTTCAAGAAACGTGTTCCAGACA 298
QY 324 CAACAAGATGAGTTTGAATCTTCACCTGTATGAGAGACACTTCTTGTGCCAAAAAGGA 383
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 297 CAACAAGATGAGTTTGAATCTTCACCTGTATGAGAGACACTTCTTGTGCCAAAAAGGA 238
QY 384 AGATGATGCTTTCAAACTCATTTCTGAAAAAAGGATGAAGATGGGATTAATCTGTAAT 443
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 237 AGATGATGCTTTCAAACTCATTTCTGAAAAAAGGATGAAGATGGGATTAATCTGTAAT 178
QY 444 GTTCACTCTCACTAATCTTACATCAAGT 471
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 177 GTTCACTCTCACTAATCTTACATCAAGT 150

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RESULT 10
A1176343/c 369 bp mRNA EST 08-JAN-1999
LOCUS
DEFINITION
EST219926 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
ROVBO38 3' end, mRNA sequence.
ACCESSION
A1176343
VERSION
A1176343.1 GI:4134870
KEYWORDS
EST.
SOURCE
Rattus sp.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS	1 (bases 1 to 369)
TITLE	Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
JOURNAL	Rat Genome Project: Generation of a Rat EST (RESt) Catalog & Rat Gene Index
COMMENT	Unpublished (1998) On Oct 8, 1998 this sequence version replaced gi:3726981. Other_ESTs: TC49330 Contact: Lee, NH ATCC
FEATURES	The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@tigr.org Seq primer: M13-21.
source	Location/Qualifiers 1..369 /organism="Rattus sp." /db_xref="taxon:10118" /clone="ROVBQ38" /clone_lib="Normalized rat ovary, Bento Soares" /note="Organ: ovary; Vector: pT7T3pac; Site_1: EcoRI; Site_2: NotI"
BASE COUNT	114 a 64 c 61 g 130 t
ORIGIN	
Query Match	44.0%; Score 207.4; DB 9; Length 369;
Best Local Similarity	91.3%; Pred. No. 6.6e-46;
Matches 220; Conservative 0; Mismatches 21; Indels 0; Gaps 0;	
QY 231	CAAGATCATTTCTCTTGAGGAATGATCCACCCTGAATAATTGATGATATACAAAGTGA 290
Db 369	CAAAATCATTTCTCTTGAGGAATGATCCACCCTGAATAATTGATGATATAAAAAGTGA 310
QY 291	TCTCATATCTTTCAGAAACGTGTTCCAGGACACACACAAGATGGAGTTGAATCTTCACT 350
Db 309	TTTCAAAATCTTTCAGAAACGTGTTCCAGGACACCAACAATGGAAATTTGAATCTTCCCT 250
QY 351	GATGAAGGACACTTCTTCTGCTGCCCCAAAAGGAAGATGATGCTTTCAAAACCTCATTCGAA 410
Db 249	GATGAAGGACCCCTTTTGTAGCTTGCCAAAAGGAAGATGATGCTTTCAAAACCTGTTTAA 190
QY 411	AAAAAAGATGAAAAATGGGATAAATCTGTAATGTTCACTCTCACTTAACCTTACATCAAAAG 470
Db 189	AAGGAAGATGAAAAATGGGATAAATCTGTAATGTTCACTCTCACTTAACCTTACATCAAAAG 130
QY 471	T 471
Db 129	T 129
RESULT 11	
LOCUS	AI835755/c
DEFINITION	AI835755 342 bp mRNA EST 14-JUL-1999
ACCESSION	UI-M-A10-aan-g-11-0-UI.s1 NIH_BMAP.MBS Mus musculus cDNA clone
VERSION	UI-M-A10-aan-g-11-0-UI 3', mRNA sequence.
KEYWORDS	AI835755
SOURCE	AI835755.1 GI:5469968
ORGANISM	EST. house mouse. Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 342)
TITLE	Bonaldo,M.F., Lennon,G. and Soares,M.B.
JOURNAL	Normalization and subtraction: two approaches to facilitate gene discovery
MEDLINE	Genome Res. 6 (9), 791-806 (1996) 97044477

COMMENT	Contact: Chin, H National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA Tel: 301 443 1706 Fax: 301 443 9890 Email: MEST@mail.nih.gov The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized brain stems library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence:: 19-78, >MSTD#LTR/MaLR Seq primer: M13 Forward POLYA=Yes.			
FEATURES	Location/Qualifiers 1..342 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UI-M-A10-aan-g-11-0-UI" /clone_lib="NIH_BMAP_MBS" /dev_stage="27-32 days" /lab_host="DH10B (Life Technologies)" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_MBS library is a non-normalized library constructed from mouse brain stems. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996. Tissue provided by Ms. Annie Novakovich, Zivic-Miller Laboratories. TAG_LIB=NIH_BMAP_MBS TAG_TISSUE=brain-stems TAG_SEQ=TCACG"			
BASE COUNT	98 a	68 c	55 g	121 t
ORIGIN				
Query Match	41.98;	Score 197.4;	DB 13;	Length 342;
Best Local Similarity	99.5%;	Pred. No. 3.2e-43;		
Matches 198;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY 273	TGATGATATACAAAGTGATCTCATATTCTTTCAGAAACGTGTTCAGACACACAACAGAT	332		
Db 342	TGATGATATACAAAGTGATCTCATATTCTTTCAGAAACGTGTTCAGACACACAACAGAT	283		
QY 333	GGAGTTGGAATCTTCACTGTATGAAGACACACTTCTCTGCGTCCCAAAAGGAAGATGATGC	392		
Db 282	GGAGTTGGAATCTTCACTGTATGAAGACACACTTCTCTGCGTCCCAAAAGGAAGATGATGC	223		
QY 393	TTTCAAACTCATTTCTGAATAAAAGGATGAATAATGGGATTAATCTGTAATGTTCACTCT	452		
Db 222	TTTCAAACTCATTTCTGAATAAAAGGATGAATAATGGGATTAATCTGTAATGTTCACTCT	163		
QY 453	CACTAACTTACATCAAAAGT 471			
Db 162	CACTAACTTACATCAAAAGT 144			
RESULT 12				
LOCUS	AV066410	335 bp	mrna	EST 24-JUN-1999
DEFINITION	AV066410 Mus musculus small intestine C57BL/6J adult Mus musculus cDNA clone 2010109E01, mRNA sequence.			
ACCESSION	AV066410			

VERSION	AV066410.1	GI:5186238
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 335) Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Nitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tomingda,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.	
TITLE	RIKEN Mouse ESTs	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Chie Owa Genome Science Laboratory RIKEN 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-9145 Fax: 81-298-36-9098 Email: genome-res@rtc.riken.go.jp Thermostabilization and thermoactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998)) Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998)) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.	
FEATURES	Location/Qualifiers	
source	1..335 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="2010109E01" /clone_lib="Mus musculus small intestine C57BL/6J adult" /sex="male" /tissue_type="small intestine" /dev_stage="adult"	
BASE COUNT	109 a 59 c 67 g 100 t	
ORIGIN		
Query Match	40.7%;	Score 191.6; DB 15; Length 335;
Best Local Similarity	95.6%;	Pred. No. 1.2e-41;
Matches 197; Conservative	0;	Mismatches 9; Indels 0; Gaps 0;
OY	266 AAAATATGATGATATACAAAGTGAATCTCATATTTCTTCAGAAACGTGTTCCAGACACA	325
Db	1 AAAATATGATCATATACAAAGTGAATCTCATATTTCTTCAGAAACCGTTCCAGACACA	60
OY	326 ACAAGAGGAGTTTGAATCTTCACTGTATGAAGGACACCTTTCTGCTGCCAAAAGGAG	385
Db	61 ACAAGATGAGTTTGAATTTTCATTTCTATGAAGGACACCTTTCTGCTGCCAAAAGGAG	120
OY	386 ATGATGCTTCAACATCATTTCTGAAGGATGAAATGGGGATTAATCTGTATGT	445
Db	121 ATGATGCTTCAACATCATTTCTGAAGGATGAAATGGGGATTAATCTGTATGT	180
OY	446 TCACCTCCTCACTTAACATCAAAAGT	471
Db	181 TCACCTCCTCACTTAACATCAAAAGT	206
RESULT 13		
LOCUS	AA245600	289 bp mRNA
DEFINITION	mx30a01.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:681672 5'	EST 10-MAR-1997
ACCESSION	AA245600	(mouse);, mRNA sequence.

VERSION	AA245600.1	GI:1876519
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 289)	
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.	
TITLE	The WashU-HMI Mouse EST Project	
JOURNAL	Unpublished (1996)	
COMMENT	Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL : contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:421376	
FEATURES	Trace considered overall poor quality Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 1.	
source	Location/Qualifiers 1..289 /organism="Mus musculus" /db_xref="taxon:10090" /clone="IMAGE:681672" /clone_lib="Soares mouse NML" /tissue_type="Liver" /lab_host="DH10B" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGGAGCGGCCGCAGATCTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."	
BASE COUNT	77 a	75 g 86 t
ORIGIN	51 c	
Query Match	36.8%;	Score 173.4; DB 2; Length 289;
Best Local Similarity	79.2%;	Pred. No. 9.5e-37;
Matches 229; Conservative	1;	Mismatches 57; Indels 2; Gaps 2;
QY	167 TAGAGGACTGCGCTGTGACCCTCCTCTGTGAAGCATAGTAATAAAGTCCTACCCCTCCTGTA	226
Ddb	1 TAGTAGGACTAGTTGTGATGCTCTGTGTGAAGCATCGTAATATGTGCATGGCGCTCGTGA	60
QY	227 AGACAAGATCATTTTCT-TTGAGGAATGATTCACCTGAAAATATTGATGATATACAA	285
Ddb	61 AGACAAGATCATTTTCTAGTAGGGAATGATACAGCTGCAATACTGACGGTATGCAC	120
QY	286 AGTGAATCTCATATTTCTTTCAGAAACGTGTTCCAGGACACACAAGAATGGAGTTGA-ATC	344
Ddb	121 AGTGATGTCAGATGCTGTACAGAACCGTGTATGAGGATGCACAAGAATGCAGTTTGACATC	180
QY	345 TTACTGTATGAGGACACTTTCTTGCTTGCCAAAAAGGAAGATGATGCTTCAAATCAT	404
Ddb	181 TGGCTCTGTCTGTGGTCACTTTCTTGCTTGTAAATAATGATGATGATGCCGTGACTCAT	240
QY	405 TCTGAAAAAAGGATGAAAAATGGGATAAATCTGTAATGTTCACTCTC	453
Ddb	241 TCTGACCAACACAGGATGATGAGGATACATCTGATGTGTCACTCTC	289

RESULT 14
AI046315 505 bp mRNA EST 08-JUL-1998
LOCUS
DEFINITION ud69c02.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1451138 5' similar to gb:D49949 Mouse mRNA for IGIF precursor
polypeptide (MOUSE);, mRNA sequence.
ACCESSION AI046315 GI:3294602
VERSION
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 505)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The Washu-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:924454
Seq primer: custom primer used
High quality sequence stop: 385.
FEATURES
source
location/Qualifiers
1..505
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1451138"
/clone_lib="Sugano mouse liver mlia"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCCTACTG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGTCTCTAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
BASE COUNT 143 a 129 c 116 g 117 t
ORIGIN
Query Match 35.4%; Score 166.8; DB 8; Length 505;
Best Local Similarity 98.8%; Pred. No. 6.8e-35;
Matches 168; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AACTTGGCCGACTTCACTGTACACCCGAGTAATACGGAATATAATGACCAAGTCTC 60
|||||
Db 336 AACTTGGCCGACTTCACTGTACACCCGAGTAATACGGAATATAATGACCAAGTCTC 395
QY 61 TTGTTGACAAAGACAGCCTGTGTTGAGGATATGACTGATATGATCAAAAGTGCCAGT 120
|||||
Db 396 TTGTTGACAAAGACAGCCTGTGTTGAGGATATGACTGATATGATCAAAAGTGCCAGT 455
QY 121 GAACCCAGACGACTGATATATATACATGTACAAAGACAGTAAGTAAG 170

Db 456 GAACCCAGACGACTGATATATATACATGTACAAAGACAGGAAGTAAG 505
|||||
RESULT 15
AV597985 574 bp mRNA EST 06-AUG-2000
LOCUS
DEFINITION AV597985 Bos taurus cartilage fetus Bos taurus cDNA clone
EICA035C10 5', mRNA sequence.
ACCESSION AV597985
VERSION AV597985.1 GI:9715480
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 574)
Sugimoto,Y., Hirotsune,S., Takasuga,A., Itoh,R., Jitohzono,A. and
Suzuki,H.
TITLE bovine cDNA sequencing
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugieco.coa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
FEATURES
source
location/Qualifiers
1..574
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="EICA035C10"
/clone_lib="Bos taurus cartilage fetus"
/tissue_type="cartilage"
/dev_stage="fetus"
/note="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A
was deleted from a NotI site"
BASE COUNT 173 a 126 c 114 g 161 t
ORIGIN
Query Match 33.0%; Score 155.6; DB 19; Length 574;
Best Local Similarity 72.9%; Pred. NO. 7.5e-32;
Matches 213; Conservative 1; Mismatches 75; Indels 3; Gaps 1;
QY 2 ACTTTGGCCGACTTCACTGTACACCGCAGTAATACGGAATATAATGACCAAGTCTCT 61
|||||
Db 280 ACTTTGGCAACTGAACTTAAGCTCTCAATCATACGAATTTGAATGACCAAGTCTCT 339
QY 62 TCGTTGACAAAGA--CAGCCTGTGTTGAGGATATGACTGATATGATCAAAAGTGCCA 118
|||||
Db 340 TCATTAACCAAGGAATCAACCTGCTTGAAGGATATGCCCTGATTCGACTGTCAGATA 399
QY 119 GTGAACCCAGACGACTGATATATATACATGTACAAAGACAGTGAAGTAGAGACTGG 178
|||||
Db 400 ATGCACCCAGACCATATTTATCATATATATATATAGGACAGCCCTCACTAGAGGCTTGG 459
QY 179 CTGTGACCCCTCTGTGTAAGGATAGTAAAAATGCTACCTCTCTGTAGAACAGATCA 238
|||||
Db 460 CCGTAACCATCTCTGTGAGGTGAAGAAATGCTACTCTCTCTGTGAGAACAAATTTG 519
QY 239 TTTCCTTTGAGAAATGATCCACCTGAAAATATGATGATATACAAAGTGA 290
|||||
Db 520 TTTCCTTTAAGAAATGATCCCTCTGATAACATTTGATATGAAGAAAGTGA 571
Search completed: November 25, 2000, 04:51:44
Job time: 3629 sec

Sat Nov 25 20:12:56 2000

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